AMENDMENTS TO THE SPECIFICATION

Please replace paragraph 0003 with the following paragraph:

Lin-4 and Let-7 each transcribe a ~22 nucleotide (nt) RNA, which acts a post transcriptional repressor of target mRNAs, by binding to elements in the 3"-untranslated region (UTR) of these target mRNAs, which are ~~complimentary~~ complementary to the 22 nt sequence of Lin-4 and Let-7 respectively. While Lin-4 and Let-7 are expressed at different developmental stage, first larval stage and fourth larval stage respectively, both specify the temporal progression of cell fates, by triggering post-transcriptional control over other genes (Wightman, B., Ha, I., Ruvkun, G., Cell 75, 855 (1993); Slack et al., Mol.Cell 5 ,659 (2000)). Let-7 as well as its temporal regulation have been demonstrated to be conserved in all major groups of bilaterally symmetrical animals, from nematodes, through flies to humans (Pasquinelli, A., et al. Nature 408 ,86 (2000)).

Please replace paragraph 0004 with the following paragraph:

The initial transcription product of Lin-4 and Let-7 is a ~60-80nt RNA, the nucleotide sequence of the first half of which is partially ~~complimentary~~ complementary to that of its second half, therefore allowing this RNA to fold onto itself, forming a "hairpin structure". The final gene product is a ~22nt RNA, which is "diced" from the above mentioned "hairpin structure", by an enzyme called Dicer, which also apparently also mediates the ~~complimentary~~ complementary binding of this ~22nt segment to a binding site in the 3" UTR of its target

gene.

Please replace paragraph 0006 with the following paragraph:

Based on the striking homology of the newly discovered MIR genes to their well-studied predecessors Lin-4 and Let-7, the new MIR genes are believed to have a similar basic function as that of Lin-4 and Let-7: modulation of target genes by ~~complimentary~~ complementary binding to the UTR of these target genes, with special emphasis on modulation of developmental control processes. This is despite the fact that the above mentioned recent studies did not find target genes to which the newly discovered MIR genes complementarily bind. While existing evidence suggests that the number of regulatory RNA genes "may turn out to be very large, numbering in the hundreds or even thousands in

each genome", detecting such genes is challenging (Ruvkun G., "Perspective: Glimpses of a tiny RNA world", Science 294 ,779 (2001)).

Please replace paragraph 0044 with the following paragraph:

Fig. 6B is a simplified flowchart illustrating training of a dicer-cut location detector constructed and operative in accordance with a preferred embodiment of the present invention; Fig. 6C is a simplified flowchart illustrating prediction of a viral genomic address messenger.

Please replace paragraph 0066 with the following paragraph:

VGAM PRECURSOR RNA folds onto itself, forming VGAM FOLDED PRECURSOR RNA. As Fig.8 illustrates, VGAM FOLDED PRECURSOR RNA forms a "hairpin structure", folding onto itself. As is well known in the art, this "hairpin structure", is typical genes of the miRNA genes, and is due to the fact that nucleotide sequence of the first half of the RNA of a gene in this group is an accurate or partial inversed-reversed sequence of the nucleotide sequence of its second half. By "inversedreversed" is meant a sequence which is reversed and wherein each nucleotide is replaced by a ~~complimentary~~ complementary nucleotide, as is well known in the art (e.g. ATGGC is the inversed-reversed sequence of GCCAT).

Please replace paragraph 0070 with the following paragraph:

The ~~complimentary~~ complementary binding of VGAM RNA to BINDING SITE inhibits translation of TARGET RNA into TARGET PROTEIN. TARGET PROTEIN is therefore outlined by a broken line.

Please replace paragraph 0071 with the following paragraph:

It is appreciated by one skilled in the art that the mode of transcriptional inhibition illustrated by Fig. 1 with specific reference to VGAM genes of the present invention, is in fact common to all other miRNA genes. A specific ~~complimentary~~ complementary binding site has been demonstrated only for Lin-4 and Let-7. All the other 93 newly discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by ~~complimentary~~ complementary binding, although specific ~~complimentary~~ complementary binding sites for these

genes have not yet been found (Ruvkun G., "Perspective: Glimpses of a tiny RNA world", Science 294 ,779 (2001)). The present invention discloses a novel group of genes, the VGAM genes, belonging to the miRNA genes group, and for which a specific an ~~complimentary~~ complementary binding has been determined.